

[illegible]

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong
Xiao

iii) NUMBER OF SEQUENCES: 23

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE: 30-Jun-1998
(C) CLASSIFICATION:

(A) NAME: Conley, Deirdre L.
(B) REGISTRATION NUMBER: 36,487
(C) REFERENCE/DOCKET NUMBER: P1084R1-1

(A) TELEPHONE: 650/225-2066
(B) TELEFAX: 650/952-9881

(A) LENGTH: 2538 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(A) NAME/KEY: mouse NRG3 nucleic acid
(B) LOCATION: 1-2538
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50
TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
GCCCCGCGCC GCGCCCGCGC CCGGCCCGCG CGGCCCCATG CCTCTGGCGC 250
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GCGGCGGGCG GCGGGGGGCC 400
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCCGGGA GTTACGCTGT 450
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTG GTTGT GCGTG GTTGCC 500
TCTGTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCACGGA CCTGGTGGAC 600
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
CCGGGTTCCT ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900
ACGCCCCGGT CCCGACCCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAACTAG 1100
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200

GAATGCTTTG	TGATTGAGAC	CCTGACAGGA	TCCCATAAGC	ACTGTCGGTG	1250
CAAGGAAGGC	TACCAAGGAG	TCCGTTGTGA	TCAATTTCTG	CCGAAAACAG	1300
ACTCCATCTT	ATCGGATCCA	ACAGACCACT	TGGGGATTGA	ATTCATGGAG	1350
AGTGAAGACG	TTTATCAAAG	GCAGGTGCTG	TCAATTTTCAT	GTATCATCTT	1400
TGGAATTGTC	ATCGTGGGCA	TGTTCTGTGC	AGCATTCTAC	TTCAAAAGCA	1450
AGAAACAAGC	TAAACAAATT	CAGGAGCACC	TGAAAGAGTC	ACAGAATGGG	1500
AAGAACTACA	GCCTCAAGGC	ATCCAGCACA	AAGTCTGAGA	GCTTGATGAA	1550
GAGCCATGTC	CATCTACAAA	ATTATTCAAA	GGCGGATAGG	CATCCTGTGA	1600
CTGCGCTGGA	GAAAATAATG	GAGTCAAGTT	TTTCAGCTCC	CCAGTCGTTC	1650
CCAGAAGTCA	CTTCTCCTGA	CCGAGGAAGC	CAGCCTATCA	AGCACCACAG	1700
CCCAGGACAA	AGGAGTGGGA	TGTTGCATAG	GAATACTTTC	AGAAGGGCAC	1750
CACCCTCACC	CCGAAGTCGA	CTGGGTGGTA	TTGTAGGACC	AGCATATCAA	1800
CAACTTGAAG	AATCAAGAAT	TCCAGACCAG	GATACGATAC	CTTGCCAAGG	1850
GATAGAGGTC	AGGAAGACTA	TATCCCACCT	GCCTATACAG	CTGTGGTGTG	1900
TTGAAAGACC	CCTGGACTTA	AAGTATGTGT	CCAATGGCTT	AAGAACCCAA	1950
CAAAATGCAT	CAATAAATAT	GCAACTGCCT	TCAAGAGAGA	CAAACCCCTA	2000
TTTTAATAGC	TTGGATCAAA	AGGACCTGGT	GGGTATTTA	TCCCCAAGGG	2050
CCAATTCTGT	GCCCATCATC	CCGTCGATGG	GTCTAGAAGA	AACCTGCATG	2100
CAAATGCCAG	GGATTTCTGA	CGTCAAAAGC	ATTAAATGGT	GCAAAAACCTC	2150
CTACTCCGCT	GACATTGTCA	ACGCGAGTAT	GCCAGTCAGT	GATTGTCTTC	2200
TAGAAGAACA	ACAGGAAGTG	AAAATATTAC	TAGAGACTGT	GCAGGAACAG	2250
ATCCGGATTC	TGACTGATGC	CAGACGGTCA	GAAGACTTCG	AACTGGCCAG	2300
CATGGAAACT	GAGGACAGTG	CGAGCGAAAA	CACAGCCTTT	CTCCCCCTGA	2350
GTCCCACGGC	CAAATCAGAA	CGAGAGGCAC	AATTTGTCTT	AAGAAATGAA	2400
ATACAAAGAG	ACTCTGTGCT	AACCAAGTGA	CTGGAAATGT	AGGAATCTGT	2450
GCATTATATG	CTTTGCTAAA	CAGGAAGGAG	AGGAAATTAA	ATACAAATTA	2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
(B) LOCATION: 1-713
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5				10						15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20				25						30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35				40						45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50				55						60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65				70						75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80				85						90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95				100						105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110				115						120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125				130						135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140				145						150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155				160						165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170				175						180	

Ser	Thr	Thr	Ala	Arg 185	Asn	Thr	Ala	Ala	Pro 190	Pro	Thr	Val	Leu	Ser 195
Thr	Thr	Ala	Pro	Phe 200	Phe	Ser	Ser	Ser	Thr 205	Pro	Gly	Ser	Arg	Pro 210
Pro	Met	Pro	Gly	Ala 215	Pro	Ser	Thr	Gln	Ala 220	Met	Pro	Ser	Trp	Pro 225
Thr	Ala	Ala	Tyr	Ala 230	Thr	Ser	Ser	Tyr	Leu 235	His	Asp	Ser	Thr	Pro 240
Ser	Trp	Thr	Leu	Ser 245	Pro	Phe	Gln	Asp	Ala 250	Ala	Ala	Ala	Ser	Ser 255
Ser	Ser	Pro	Ser	Ser 260	Thr	Ser	Ser	Thr	Thr 265	Thr	Thr	Pro	Glu	Thr 270
Ser	Thr	Ser	Pro	Lys 275	Phe	His	Thr	Thr	Thr 280	Tyr	Ser	Thr	Glu	Arg 285
Ser	Glu	His	Phe	Lys 290	Pro	Cys	Arg	Asp	Lys 295	Asp	Leu	Ala	Tyr	Cys 300
Leu	Asn	Asp	Gly	Glu 305	Cys	Phe	Val	Ile	Glu 310	Thr	Leu	Thr	Gly	Ser 315
His	Lys	His	Cys	Arg 320	Cys	Lys	Glu	Gly	Tyr 325	Gln	Gly	Val	Arg	Cys 330
Asp	Gln	Phe	Leu	Pro 335	Lys	Thr	Asp	Ser	Ile 340	Leu	Ser	Asp	Pro	Thr 345
Asp	His	Leu	Gly	Ile 350	Glu	Phe	Met	Glu	Ser 355	Glu	Asp	Val	Tyr	Gln 360
Arg	Gln	Val	Leu	Ser 365	Ile	Ser	Cys	Ile	Ile 370	Phe	Gly	Ile	Val	Ile 375
Val	Gly	Met	Phe	Cys 380	Ala	Ala	Phe	Tyr	Phe 385	Lys	Ser	Lys	Lys	Gln 390
Ala	Lys	Gln	Ile	Gln 395	Glu	His	Leu	Lys	Glu 400	Ser	Gln	Asn	Gly	Lys 405
Asn	Tyr	Ser	Leu	Lys 410	Ala	Ser	Ser	Thr	Lys 415	Ser	Glu	Ser	Leu	Met 420
Lys	Ser	His	Val	His 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Ala	Asp	Arg	His 435

Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile
695 700 705

Gln Arg Asp Ser Val Leu Thr Lys
710 713

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro				

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(2) INFORMATION FOR SEQ ID NO:4:

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn
 1             5             10             15
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys
                20             25             30
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln
                35             40             45
Phe Leu
 47
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
- (B) LOCATION: 1-2502
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50
GAGCCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100
GCCGCGGCCC TCGGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150
AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200
TCGGCCGAGG AGGGCACCGC GCGGGCTGCG GCGGCGGCAG CGGCGGGCGG 250
GGGCCCCGAC GCGGGCGGCG AAGGGGCGGC CGAGCCCCCC CGGGAGTTAC 300
GCTGTAGCGA CTGCATCGTG TGGAACCGGC AGCAGACGTG GCTGTGCGTG 350
GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400
```

CAAATGGATC	GTGGTGGGCT	CCGTCAAGGA	GTACGTGCCC	ACCGACCTAG	450
TGGACTCCAA	GGGGATGGGC	CAGGACCCCT	TCTTCCTCTC	CAAGCCCAGC	500
TCTTTCCCCA	AGGCCATGGA	GACCACCACC	ACTACCACTT	CCACCACGTC	550
CCCCGCCACC	CCCTCCGCCG	GGGGTGCCGC	CTCCTCCAGG	ACGCCCAACC	600
GGATTAGCAC	TCGCCTGACC	ACCATCACGC	GGGCGCCCAC	TCGCTTCCCC	650
GGGCACCGGG	TGCCCATCCG	GGCCAGCCCG	CGCTCCACCA	CAGCACGGAA	700
CACTGCGGCC	CCTGCGACGG	TCCCGTCCAC	CACGGCCCCG	TTCTTCAGTA	750
GCAGCACGCT	GGGCTCCCGA	CCCCCGGTGC	CAGGAACTCC	AAGTACCCAG	800
GCAATGCCCT	CCTGGCCTAC	TGCGGCATAC	GCTACCTCCT	CCTACCTTCA	850
CGATTCTACT	CCCTCCTGGA	CCCTGTCTCC	CTTTCAGGAT	GCTGCCTCCT	900
CTTCTTCCTC	TTCTTCCTCC	TCCGCTACCA	CCACCACACC	AGAAACTAGC	950
ACCAGCCCCA	AATTTCATAC	GACGACATAT	TCCACAGAGC	GATCCGAGCA	1000
CTTCAAACCC	TGCCGAGACA	AGGACCTTGC	ATACTGTCTC	AATGATGGCG	1050
AGTGCTTTGT	GATCGAAACC	CTGACCGGAT	CCCATAAACA	CTGTCGGTGC	1100
AAAGAAGGCT	ACCAAGGAGT	CCGTTGTGAT	CAATTTCTGC	CGAAAACTGA	1150
TTCCATCTTA	TCGGATCCAA	CAGACCACTT	GGGGATTGAA	TTCATGGAGA	1200
GTGAAGAAGT	TTATCAAAGG	CAGGTGCTGT	CAATTTCATG	TATCATCTTT	1250
GGAATTGTCA	TCGTGGGCAT	GTTCTGTGCA	GCATTCTACT	TCAAAGCAA	1300
GAAACAAGCT	AAACAAATCC	AAGAGCAGCT	GAAAGTGCCA	CAAAATGGTA	1350
AAAGCTACAG	TCTCAAAGCA	TCCAGCACAA	TGGCAAAGTC	AGAGAACTTG	1400
GTGAAGAGCC	ATGTCCAGCT	GCAAAATTAT	TCAAAGGTGG	AAAGGCATCC	1450
TGTGACTGCA	TTGGAGAAAA	TGATGGAGTC	AAGTTTTGTC	GGCCCCCAGT	1500
CATTCCCTGA	GGTCCCTTCT	CCTGACAGAG	GAAGCCAGTC	TGTCAAACAC	1550
CACAGGAGTC	TATCCTCTTG	CTGCAGCCCA	GGGCAAAGAA	GTGGCATGCT	1600
CCATAGGAAT	GCCTTCAGAA	GGACACCCCC	GTCACCCCGA	AGTAGGCTAG	1650
GTGGAATTGT	GGGACCAGCA	TATCAGCAAC	TCGAAGAATC	AAGGATCCCA	1700

GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750
 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800
 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850
 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900
 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950
 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000
 AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050
 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100
 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150
 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200
 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250
 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300
 AAGTGACTION AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350
 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400
 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450
 TTAACAAAAT ATTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500
 TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser
1				5					10					15

Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala		20	25	30
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala		35	40	45
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp		50	55	60
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly		65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val		80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser		95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser		110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr		125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr		140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro		155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg		170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser		185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro		200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro		215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro		230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser		245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr		260	265	270

Overall mean (SD)		Overall range	
Age (years)	22.5 (2.0)	18-30	18-30
Gender			
Male	10 (50.0)	10	10
Female	10 (50.0)	10	10
Marital status			
Married	10 (50.0)	10	10
Single	10 (50.0)	10	10
Education			
High school	10 (50.0)	10	10
University	10 (50.0)	10	10
Occupation			
Student	10 (50.0)	10	10
Worker	10 (50.0)	10	10
Unemployed	10 (50.0)	10	10
Family size			
1-2	10 (50.0)	10	10
3-4	10 (50.0)	10	10
5-6	10 (50.0)	10	10
7-8	10 (50.0)	10	10
9-10	10 (50.0)	10	10
11-12	10 (50.0)	10	10
13-14	10 (50.0)	10	10
15-16	10 (50.0)	10	10
17-18	10 (50.0)	10	10
19-20	10 (50.0)	10	10
21-22	10 (50.0)	10	10
23-24	10 (50.0)	10	10
25-26	10 (50.0)	10	10
27-28	10 (50.0)	10	10
29-30	10 (50.0)	10	10
31-32	10 (50.0)	10	10
33-34	10 (50.0)	10	10
35-36	10 (50.0)	10	10
37-38	10 (50.0)	10	10
39-40	10 (50.0)	10	10
41-42	10 (50.0)	10	10
43-44	10 (50.0)	10	10
45-46	10 (50.0)	10	10
47-48	10 (50.0)	10	10
49-50	10 (50.0)	10	10
51-52	10 (50.0)	10	10
53-54	10 (50.0)	10	10
55-56	10 (50.0)	10	10
57-58	10 (50.0)	10	10
59-60	10 (50.0)	10	10
61-62	10 (50.0)	10	10
63-64	10 (50.0)	10	10
65-66	10 (50.0)	10	10
67-68	10 (50.0)	10	10
69-70	10 (50.0)	10	10
71-72	10 (50.0)	10	10
73-74	10 (50.0)	10	10
75-76	10 (50.0)	10	10
77-78	10 (50.0)	10	10
79-80	10 (50.0)	10	10
81-82	10 (50.0)	10	10
83-84	10 (50.0)	10	10
85-86	10 (50.0)	10	10
87-88	10 (50.0)	10	10
89-90	10 (50.0)	10	10
91-92	10 (50.0)	10	10
93-94	10 (50.0)	10	10
95-96	10 (50.0)	10	10
97-98	10 (50.0)	10	10
99-100	10 (50.0)	10	10
101-102	10 (50.0)	10	10
103-104	10 (50.0)	10	10
105-106	10 (50.0)	10	10
107-108	10 (50.0)	10	10
109-110	10 (50.0)	10	10
111-112	10 (50.0)	10	10
113-114	10 (50.0)	10	10
115-116	10 (50.0)	10	10
117-118	10 (50.0)	10	10
119-120	10 (50.0)	10	10
121-122	10 (50.0)	10	10
123-124	10 (50.0)	10	10
125-126	10 (50.0)	10	10
127-128	10 (50.0)	10	10
129-130	10 (50.0)	10	10
131-132	10 (50.0)	10	10
133-134	10 (50.0)	10	10
135-136	10 (50.0)	10	10
137-138	10 (50.0)	10	10
139-140	10 (50.0)	10	10
141-142	10 (50.0)	10	10
143-144	10 (50.0)	10	10
145-146	10 (50.0)	10	

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: cARIA.egf
 (B) LOCATION: 1-48
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn
 1 5 10 15
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg
 20 25 30
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
 35 40 45
Asn Tyr Val
 48

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hAR.egf
 (B) LOCATION: 1-45
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
 1 5 10 15
Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
 20 25 30
Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hBTC.efg
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 5 10 15
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val
20 25 30
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hEGF.egf
(B) LOCATION: 1-46
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
20 25 30
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
35 40 45
Leu
46

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHB-EGF.egf
- (B) LOCATION: 1-45
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile
20 25 30
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGalpha.egf
- (B) LOCATION: 1-49
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr
35 40 45
Glu Asn Tyr Pro
49

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His
1 5 10 15
Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val
20 25 30
Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mEPR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Ile Thr Lys Cys Ser Ser Asp Met Asp Gly Tyr Cys Leu His
1 5 10 15
Gly Gln Cys Ile Tyr Leu Val Asp Met Arg Glu Lys Phe Cys Arg
20 25 30
Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys Glu His Phe Phe Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Oligonucleotide probe
(B) LOCATION: 1-50
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly
1 5 10 15
Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly
20 25 30
Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys
35 40 45
Ala Gly Ala Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 1
(B) LOCATION: 1-8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Asp Gly Glu Cys Phe Val Ile
1 5 8

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 2
(B) LOCATION: 1-9
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Phe Met Glu Ser Glu Glu Val Tyr
1 5 9

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: EST Genbank entry H23651
(B) LOCATION: 1-466
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100
AATTTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150
CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTTNTGAT GACATTTNCA 400
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450
TTTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2091 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTTGCGCAGC 50
CGCCGCCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100
CGGGCGGGGG CCCGGACGGC GCGGCGGAAG GGGCGGCCGA GGGGGGGGG 150
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCACC 300
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCCAA 350
GCCCAGCTCT TTCCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450

CCCAACCGGA	TTAGCACTCG	CCTGACCACC	ATCACGCGGG	CGCCCACTCG	500
CTTCCCCGGG	CACCGGGTGC	CCATCCGGGC	CAGCCCGCGC	TCCACCACAG	550
CACGGAACAC	TGCGGCCCCT	GCGACGGTCC	CGTCCACCAC	GGCCCCGTTC	600
TTCAGTAGCA	GCACGCTGGG	CTCCCGACCC	CCGGTGCCAG	GAACTCCAAG	650
TACCCAGGCA	ATGCCCTCCT	GGCCTACTGC	GGCATA CGCT	ACCTCCTCCT	700
ACCTTCACGA	TTCTACTCCC	TCCTGGACCC	TGTCTCCCTT	TCAGGATGCT	750
GCCTCCTCTT	CTTCCTCTTC	TTCCTCCTCC	GCTACCACCA	CCACACCAGA	800
AACTAGCACC	AGCCCCAAAT	TTCATACGAC	GACATATTCC	ACAGAGCGAT	850
CCGAGCACTT	CAAACCCTGC	CGAGACAAGG	ACCTTGCATA	CTGTCTCAAT	900
GATGGCGAGT	GCTTTGTGAT	CGAAACCCTG	ACCGGATCCC	ATAAACACTG	950
TCGGTGCAAA	GAAGGCTACC	AAGGAGTCCG	TTGTGATCAA	TTTCTGCCGA	1000
AAACTGATTC	CATCTTATCG	GATCCAACAG	ACCACTTGGG	GATTGAATTC	1050
ATGGAGAGTG	AAGAAGTTTA	TCAAAGGCAG	GTGCTGTCAA	TTTCATGTAT	1100
CATCTTTGGA	ATTGTCATCG	TGGGCATGTT	CTGTGCAGCA	TTCTACTTCA	1150
AAAGCAAGAA	ACAAGCTAAA	CAAATCCAAG	AGCAGCTGAA	AGTGCCACAA	1200
AATGGTAAAA	GCTACAGTCT	CAAAGCATCC	AGCACAATGG	CAAAGTCAGA	1250
GAACTTGGTG	AAGAGCCATG	TCCAGCTGCA	AAATTATTCA	AAGGTGGAAA	1300
GGCATCCTGT	GACTGCATTG	GAGAAAATGA	TGGAGTCAAG	TTTTGTCTGC	1350
CCCCAGTCAT	TCCCTGAGGT	CCCTTCTCCT	GACAGAGGAA	GCCAGTCTGT	1400
CAAACACCAC	AGGAGTCTAT	CCTCTTGCTG	CAGCCCAGGG	CAAAGAAGTG	1450
GCATGCTCCA	TAGGAATGCC	TTCAGAAGGA	CACCCCCGTC	ACCCCGAAGT	1500
AGGCTAGGTG	GAATTGTGGG	ACCAGCATAT	CAGCAACTCG	AAGAATCAAG	1550
GATCCCAGAC	CAGGATACGA	TACCTTGCCA	AGGGTATTCA	TCCAGTGGTT	1600
TAAAAACCCA	ACGAAATACA	TCAATAAATA	TGCAACTGCC	TTCAAGAGAG	1650
ACAAACCCCT	ATTTTAATAG	CTTGAGACAA	AAGGACCTGG	TGGGCTATTC	1700
ATCCACAAGG	GCCAGTTCTG	TGCCCATCAT	CCCTTCAGTG	GGTTTAGAGG	1750

AAACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAG CATCAAATGG 1800
 TGCAAAACT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850
 CGATTGTCTT ATAGCAGAAC AACAGAAGT GAAAATATTG CTAGAACTG 1900
 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950
 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGCGAAA ACACAGCCTT 2000
 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050
 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	

Met Phe Cys Ala	Ala Phe Tyr Phe Lys	Ser Lys Lys Gln Ala	Lys
	380	385	390
Gln Ile Gln Glu	Gln Leu Lys Val Pro	Gln Asn Gly Lys Ser	Tyr
	395	400	405
Ser Leu Lys Ala	Ser Ser Thr Met Ala	Lys Ser Glu Asn Leu	Val
	410	415	420
Lys Ser His Val	Gln Leu Gln Asn Tyr	Ser Lys Val Glu Arg	His
	425	430	435
Pro Val Thr Ala	Leu Glu Lys Met Met	Glu Ser Ser Phe Val	Gly
	440	445	450
Pro Gln Ser Phe	Pro Glu Val Pro Ser	Pro Asp Arg Gly Ser	Gln
	455	460	465
Ser Val Lys His	His Arg Ser Leu Ser	Ser Cys Cys Ser Pro	Gly
	470	475	480
Gln Arg Ser Gly	Met Leu His Arg Asn	Ala Phe Arg Arg Thr	Pro
	485	490	495
Pro Ser Pro Arg	Ser Arg Leu Gly Gly	Ile Val Gly Pro Ala	Tyr
	500	505	510
Gln Gln Leu Glu	Glu Ser Arg Ile Pro	Asp Gln Asp Thr Ile	Pro
	515	520	525
Cys Gln Gly Tyr	Ser Ser Ser Gly Leu	Lys Thr Gln Arg Asn	Thr
	530	535	540
Ser Ile Asn Met	Gln Leu Pro Ser Arg	Glu Thr Asn Pro Tyr	Phe
	545	550	555
Asn Ser Leu Glu	Gln Lys Asp Leu Val	Gly Tyr Ser Ser Thr	Arg
	560	565	570
Ala Ser Ser Val	Pro Ile Ile Pro Ser	Val Gly Leu Glu Glu	Thr
	575	580	585
Cys Leu Gln Met	Pro Gly Ile Ser Glu	Val Lys Ser Ile Lys	Trp
	590	595	600
Cys Lys Asn Ser	Tyr Ser Ala Asp Val	Val Asn Val Ser Ile	Pro
	605	610	615
Val Ser Asp Cys	Leu Ile Ala Glu Gln	Gln Glu Val Lys Ile	Leu
	620	625	630

Leu	Glu	Thr	Val	Gln	Glu	Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg
				635					640					645
Arg	Ser	Glu	Asp	Tyr	Glu	Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser
				650					655					660
Ala	Ser	Glu	Asn	Thr	Ala	Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys
				665					670					675
Ser	Glu	Arg	Glu	Ala	Gln	Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg
				680					685					690
Asp	Ser	Ala	Leu	Thr	Lys									
				695	696									